

**REMARKS**

Claims 1, 13-20, and 23-24 are pending and under consideration. Claims 2-10 have been canceled without prejudice as non-elected claims. Claims 21-22 have been canceled without prejudice. Claims 1, 13 and 17 have been amended. The claim amendments herein are for clarification purposes or to correct typographical errors. The subject matter claimed in new claims 23-24 was disclosed by Figure 1 of the originally filed specification. Therefore, none of the amendments presented herein are narrowing amendments, and no new matter has been presented.

**Claim Rejection Under 35 U.S.C. §112, Second Paragraph**

Claims 1 and 13-22 have been rejected under 35 U.S.C. §112, second paragraph, as allegedly failing to particularly point out and distinctly claim the subject matter which the applicants regard as the invention. The Office Action alleges that claims 1 and 13 are vague and indefinite in the recitation of certain positions in the 16S rRNA without an indication of the context of these positions. The Office Action alleges that the intended sequences must be in the specification and/or claims in proper form for examination. This rejection is respectfully traversed.

Claims 1 and 13 have been amended and now require that the position numbers "correspond to the *E. coli* numbering system." It is respectfully submitted that this limitation makes the claims very clear and definite, for the following reasons.

The use of the *Escherichia coli* 16S rRNA gene sequence as an alignment reference has been traditionally used after techniques have been developed using the 16S rRNA gene sequence for characterization of prokaryotes. The use of the *E. coli* numbering system and the importance of aligning regions of homology within a 16S rRNA gene sequence are explained in a frequently cited paper, a copy of which is attached herewith for the Examiner's easy reference. See, Lane, et al., Proc. Natl. Acad. Sci. USA, vol. 82 (1985), pp. 6955-6959.

The following example can be provided in order to further illustrate how the *E. coli* sequence is used in an alignment. In this example, a reference sequence of *E. coli* can be chosen from the Ribosomal Database Project (RDP) described in Cole, et al., *Nucleic Acids Research*, vol. 31, No. 1 (2003), pp. 423-443, a copy of which is attached for the Examiner's easy reference.

The RDP maintains ribosomal sequence alignments which take into account secondary structure and areas of homology within the 16S rRNA gene and adjusts for hypervariable regions by aligning an entire 16S ribosomal RNA gene sequence (generally about 1500 nucleotides) over 4182 possible positions. This is an automated operation that is clear and straightforward to one skilled in the art of prokaryotic phylogenetics. Using the online alignment tool in the PHYLIP interface on the RDP website (<http://rdp.cme.msu.edu/cgis/phylip.cgi>), *Salinospora* (MAR1) and *E. coli* 16S rRNA gene sequences were uploaded and nucleotide positions were calculated automatically. The positional relationships are summarized in Table 1 and shown in detail in the attached supplementary files.

Table 1

<i>Salinospora</i> (MAR1) Signature Nucleotide Using <i>E. coli</i> Numbering System	Other <i>Micromonosporaceae</i> Family Members	<i>Salinospora</i> (MAR1) Signature Nucleotide	Position of <i>Salinospora</i> (MAR1) Signature Nucleotide Using RDP Alignment
207	T/C	A	713
366	A/G	C	1043
467	A/G	T	1221
468	A	T	1222
1456	A	G	3619

As seen from Table 1, the first *Salinospora* (MAR1) signature nucleotide occurs at nucleotide position 207 in the *E. coli* sequence. When aligned by the automated system in the RDP, the same nucleotide 207 shares the space 713 (see also the supplementary files). For further information regarding Table 1, see Mincer, et al., *Appl Environ Microbiol*, 68(10) (2002) pp. 5005-5011.

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The supplementary text files are further enclosed to illustrate each of the signatures enclosed in quotation marks (“ ”) with no spaces. Also included are the same sequence files in the text form of the alignments (including spaces). To illustrate further, the *Salinospora* (MAR1) signature nucleotide relationship to *E. coli* and the RDP alignment convention sequences have also been included in a typical alignment viewer in RDP format over 4182 positions that is easier to compare (note that each signature has been highlighted).

In view of the foregoing, it can be stated that in context of the alignment using the *E. coli* numbering system, the recitation of certain positions in the 16S rRNA is definite. It is, therefore, respectfully submitted that claims are now clear and unambiguous. Accordingly, Applicants request withdrawal of the rejection of claims 1 and 13-20 under 35 U.S.C. §112, second paragraph.

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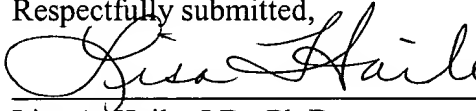
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**CONCLUSION**

In view of the amendments and the above remarks, it is submitted that the claims are in condition for allowance and a notice to that effect is respectfully requested. The Examiner is invited to contact Applicant's undersigned representative if there are any questions relating to this application. Please charge any additional fees, or make any credits, to Deposit Account No. 50-1355.

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Respectfully submitted,



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